

SEQUENCE LISTING

<110> Susan Gregory

<120> MOUSE MODEL FOR BONE METABOLISM

<130> 23546-08149/BIOL0019US

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<223> Antisense Oligonucleotide

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 cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag 180
 cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg 229
 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
 1 5 10 15
 gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277
 Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His

20	25	30	
gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc			325
Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser			
35	40	45	
atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc			373
Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser			
50	55	60	
gtc gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata			421
Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile			
65	70	75	
tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa			469
Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu			
80	85	90	95
aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta			517
Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu			
100	105	110	
ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg			565
Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val			
115	120	125	
caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag			613
Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu			
130	135	140	
aaa gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag			661
Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys			
145	150	155	
ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc			709
Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile			
160	165	170	175
cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg			757

Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg
180 185 190

ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata 805
Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile
195 200 205

ggt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga 853
Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
210 215 220

cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg 901
His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met
225 230 235

gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg 949
Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu
240 245 250 255

atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat 997
Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His
260 265 270

ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag 1045
Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu
275 280 285

gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag 1093
Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
290 295 300

gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat tga 1138
Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
305 310 315

gccccagttt ttggagtgtt atgtatttcc tggatgtttg gaaacatttt ttaaaacaag 1198

ccaagaaaga tgtatatagg tgtgtgagac tactaagagg catggcccca acggtacacg 1258

actcagtatc catgctcttg accttgtaga gaacacgcgt atttacagcc agtgggagat 1318

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agcaggatgt tggccaccag gtgcctttca aatttagaaa ctaattgact ttagaaagct 1978

gacattgcca aaaaggatac ataatgggcc actgaaatct gtcaagagta gttatataat 2038

tgttgaacag gtgtttttcc acaagtgccg caaattgtac cttttttttt ttttcaaaat 2098

agaaaagtta ttagtggttt atcagcaaaa aagtccaatt ttaatttagt aaatgttatc 2158

ttatactgta caataaaaac attgcctttg aatgttaatt ttttggtaca aaaataaatt 2218

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tggtgcttcc tcctttcatc a

21

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31

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19

<210> 9

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<220>

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<211> 20

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<220>

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<400> 10

caagcttccc gttctcagcc

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<213> M. musculus

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<222> (142)...(1092)

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ccgaactccg ggcgccgcgc c atg cgc cgg gcc agc cga gac tac ggc aag 171

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys

1 5 10

tac ctg cgc agc tcg gaa gag atg ggc agc ggc ccc ggc gtc cca cac 219

Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His

15 20 25

gaa ggt ccg ctg cac ccc gcg cct tct gca ccg gct ccg gcg ccg cca 267

Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro

30 35 40

ccc gcc gcc tcc cgc tcc atg ttc ctg gcc ctc ctg ggg ctg gga ctg 315

Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu

45 50 55

ggc cag gtg gtc tgc agc atc gct ctg ttc ctg tac ttt cga gcg cag 363

Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln

60 65 70

atg gat cct aac aga ata tca gaa gac agc act cac tgc ttt tat aga 411

Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg

75 80 85 90

atc ctg aga ctc cat gaa aac gca ggt ttg cag gac tcg act ctg gag 459

Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu

95 100 105

agt gaa gac aca cta cct gac tcc tgc agg agg atg aaa caa gcc ttt 507
Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe
110 115 120

cag ggg gcc gtg cag aag gaa ctg caa cac att gtg ggg cca cag cgc 555
Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg
125 130 135

ttc tca gga gct cca gct atg atg gaa ggc tca tgg ttg gat gtg gcc 603
Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala
140 145 150

cag cga ggc aag cct gag gcc cag cca ttt gca cac ctc acc atc aat 651
Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn
155 160 165 170

gct gcc agc atc cca tcg ggt tcc cat aaa gtc act ctg tcc tct tgg 699
Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp
175 180 185

tac cac gat cga ggc tgg gcc aag atc tct aac atg acg tta agc aac 747
Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn
190 195 200

gga aaa cta agg gtt aac caa gat ggc ttc tat tac ctg tac gcc aac 795
Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn
205 210 215

att tgc ttt cgg cat cat gaa aca tcg gga agc gta cct aca gac tat 843
Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr
220 225 230

ctt cag ctg atg gtg tat gtc gtt aaa acc agc atc aaa atc cca agt 891
Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser
235 240 245 250

tct cat aac ctg atg aaa gga ggg agc acg aaa aac tgg tcg ggc aat 939
Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn

255	260	265	
tct gaa ttc cac ttt tat tcc ata aat gtt ggg gga ttt ttc aag ctc			987
Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu			
270	275	280	
cga gct ggt gaa gaa att agc att cag gtg tcc aac cct tcc ctg ctg			1035
Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu			
285	290	295	
gat ccg gat caa gat gcg acg tac ttt ggg gct ttc aaa gtt cag gac			1083
Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp			
300	305	310	
ata gac tga gactcatttc gtggaacatt agcatggatg tcctagatgt ttggaaactt			1142
Ile Asp			
315			
cttaaaaaat ggatgatgtc tatacatgtg taagactact aagagacatg gccacgggtg			1202
tatgaaactc acagccctct ctcttgagcc ctgtacaggt tgtgtatatg taaagtccat			1262
aggtgatgtt agattcatgg tgattacaca acggttttac aattttgtaa tgatttccta			1322
gaattgaacc agattgggag aggtattccg atgcttatga aaaacttaca cgtgagctat			1382
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aaggTactcg tagctaaggg ggcagaatac tgTttctggT gaccacatgt agTttatttc			1802

tttattcttt ttaacttaat agagtcttca gacttggtcaa aactatgcaa gcaaaataaa 1862
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tcaaatttag aagctaattg actttaggag ctgacatagc caaaaaggaa cataataggc 1982
tactgaaatc tgtcaggagt atttatgcaa ttattgaaca ggtgtctttt ttacaagag 2042
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aaaaaaaaaa aaaaaa 2237

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aagcagtgag tgctgtcttc tga

23

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<211> 28

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tttcgagcgc agatggatcc taacagaa

28

<210> 15

<211> 20

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15

gag atg ggc agt tgc cct ggc gtc cca cac gag ggt ccg ctg cat ccc

96

Glu Met Gly Ser Cys Pro Gly Val Pro His Glu Gly Pro Leu His Pro

20

25

30

gcg cct tca gca ccg gct cca gcg ccg ccc ccc gcc gcc tcc cgc ttc

144

Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Phe	
35 40 45	
atg ttc ctg gcg ctc ctg ggg ctg gga ctg ggt cag gtg gtc tgc agc	192
Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser	
50 55 60	
atc gct ctg ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata	240
Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	
65 70 75 80	
tca gaa gac agc acg cgc tgc ttc tac aga att ctg aga ctc cgt gaa	288
Ser Glu Asp Ser Thr Arg Cys Phe Tyr Arg Ile Leu Arg Leu Arg Glu	
85 90 95	
aat aca ggt ttg cag gac tcg act ctg gag agc gaa gac aca gaa gca	336
Asn Thr Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Glu Ala	
100 105 110	
cta cct gac tca tgc agg aga atg aaa caa gcc ttt caa ggg gcc gtg	384
Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val	
115 120 125	
caa agg gaa tta caa cac att gtg ggg cca cag cgc ttc tca gga gtt	432
Gln Arg Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Val	
130 135 140	
cca gct atg atg gaa ggt tcg tgg ctc gat gtg gcc cgg cgg ggc aag	480
Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Arg Arg Gly Lys	
145 150 155 160	
cct gag gct cag ccg ttt gct cac ctc acc atc aat gct gcc gac atc	528
Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Asp Ile	
165 170 175	
cca tcg ggt tcc cat aaa gtc agt ctg tcc tct tgg tac cat gat cga	576
Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg	
180 185 190	

ggc tgg gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg 624
Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg
195 200 205

gtt aac caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttc agg 672
Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
210 215 220

cat cat gaa acc tca ggg agc gta cct gcg gac tat ctt cag ctg atg 720
His His Glu Thr Ser Gly Ser Val Pro Ala Asp Tyr Leu Gln Leu Met
225 230 235 240

gta tat gtc gtt aaa acc agc atc aaa atc cca agt tcg cat aac ctg 768
Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu
245 250 255

atg aaa ggg ggg agc act aag aac tgg tca ggg aat tct gaa ttc cac 816
Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His
260 265 270

ttt tat tcc ata aac gtt gga gga ttt ttc aag ctc cgg gct ggt gag 864
Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu
275 280 285

gaa att agc gtc cag gtg tcc aac cct tcc ctg ttg gat ccg gat caa 912
Glu Ile Ser Val Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
290 295 300

gat gcg acg tac ttt ggg gct ttc aaa gtt caa gac ata gac tga 957
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957

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<400> 21

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ttgtgcagtg ccagcctcgt ctca

24

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ccgagctcgg taccaagctt

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<223> Antisense Oligonucleotide

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<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 27

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<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 28

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20

<210> 29

<211> 20

<212> DNA

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<223> Antisense Oligonucleotide

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<210> 30

<211> 20

<212> DNA

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<210> 31

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cccagcccca ggagggccac

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acgctgcaga caacctggcc

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cgctctgaaa tagaagaaca

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tctgatattc tattaggatc

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gaaaatctgc attttcatgg

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<400> 42

agagttgtgt cttgaaaatc

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<212> DNA

<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 44

gaatcaggta ttaattttgt

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<210> 45

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<223> Antisense Oligonucleotide

<400> 45

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